

m. Pak

#8000

1646

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/199,874DATE: 03/10/2000  
TIME: 15:41:06

Input Set: I199874.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

P.S

ENTERED

RECEIVED  
MAR 27 2000  
TC 1600 MAIL ROOM

<110> APPLICANT: Segre, Gino V.  
Kronenberg, Henry M.  
Abou-Samra, Abdul-Badi  
Juppner, Harald  
Potts, Jr., John T.  
Schipani, Ernestina  
<120> TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME  
<130> FILE REFERENCE: 00786/071005  
<140> CURRENT APPLICATION NUMBER: US/09/199,874  
<141> CURRENT FILING DATE: 1998-11-24  
<150> EARLIER APPLICATION NUMBER: US 08/471,494  
<151> EARLIER FILING DATE: 1995-06-06  
<160> NUMBER OF SEQ ID NOS: 21  
<170> SOFTWARE: FastSEQ for Windows Version 4.0  
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<212> TYPE: DNA  
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Met Gly Ala Pro Arg Ile  
1 5

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Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val  
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Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile  
25 30 35

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40 45 50

gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca 307  
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser  
55 60 65 70

agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc 355  
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro  
75 80 85

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Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp  
90 95 100

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**RAW SEQUENCE LISTING**  
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Input Set: I199874.RAW

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47	105 110 115	
48	gtg ccc ggc aag gtg gtg gcc gtg ccc tgc ccc gac tac ttc tac gac	499
49	Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp	
50	120 125 130	
51	ttc aac cac aaa ggc cga gcc tat cgg cgc tgt gac agc aat ggc agc	547
52	Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser	
53	135 140 145 150	
54	tgg gag ctg gtg cct ggg aac aac cgg aca tgg gcg aat tac agc gaa	595
55	Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu	
56	155 160 165	
57	tgt gtc aag ttt ctg acc aac gag acc cgg gaa cgg gaa gtc ttt gat	643
58	Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp	
59	170 175 180	
60	cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc	691
61	Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser	
62	185 190 195	
63	ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc	739
64	Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys	
65	200 205 210	
66	acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg	787
67	Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg	
68	215 220 225 230	
69	gct gta agc atc ttc atc aag gat gct gtg ctc tac tgc ggg gtt tcc	835
70	Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser	
71	235 240 245	
72	aca gat gaa atc gag cgc atc acc gag gag gag ctg agg gcc ttc aca	883
73	Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr	
74	250 255 260	
75	gag cct ccc cct gct gac aag gcg ggt ttt gtg ggc tgc aga gtg gcg	931
76	Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala	
77	265 270 275	
78	gta acc gtc ttc ctt tac ttc ctg acc acc aac tac tac tgg atc ctg	979
79	Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu	
80	280 285 290	
81	gtg gaa ggc ctc tac ctt cac agc ctc atc ttc atg gct ttt ttc tct	1027
82	Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser	
83	295 300 305 310	
84	gag aaa aag tat ctc tgg ggt ttc aca tta ttt ggc tgg ggc ctc cct	1075
85	Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro	
86	315 320 325	
87	gcc gtg ttt gtc gct gtg tgg gtg acc gtg agg gct aca ctg gcc aac	1123
88	Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn	
89	330 335 340	
90	act gag tgc tgg gac ctg agt tgc ggg aat aag aaa tgg atc ata cag	1171
91	Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln	
92	345 350 355	
93	gtg ccc atc ctg gca gct att gtg gtg aac ttt att ctt ttt atc aat	1219
94	Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn	

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98  375          380          385          390
99  tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc      1315
100  cys asp thr arg gln gln tyr arg lys leu leu lys ser thr leu val
101          395          400          405
102  ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg      1363
103  leu met pro leu phe gly val his tyr ile val phe met ala thr pro
104          410          415          420
105  tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa      1411
106  tyr thr glu val ser gly ile leu trp gln val gln met his tyr glu
107          425          430          435
108  atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt      1459
109  met leu phe asn ser phe gln gly phe phe val ala ile ile tyr cys
110          440          445          450
111  ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga      1507
112  phe cys asn gly glu val gln ala glu ile lys lys ser trp ser arg
113  455          460          465          470
114  tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt      1555
115  trp thr leu ala leu asp phe lys arg lys ala arg ser gly ser ser
116          475          480          485
117  acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg      1603
118  thr tyr ser tyr gly pro met val ser his thr ser val thr asn val
119          490          495          500
120  gga cct cga ggg ggc tgg cct tgt ccc tca gcc ctc gac tagctcctgg      1652
121  gly pro arg gly gly trp pro cys pro ser ala leu asp
122          505          510          515
123  ggctggagcc agtgccaatg gccatcacca gttgcctggc tatgtgaagc atgggtccat      1712
124  ttctgagaac tcattgcctt catctggccc agagcctggc accaaagatg acgggtatct      1772
125  caatggctct ggactttatg agccaatggt tggggaacag cccctccac tcctggagga      1832
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127  <210> SEQ ID NO 2
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137  Met Gly Ala Pro Arg Ile
138  1 5
139  tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc      163
140  ser his ser leu ala leu leu leu cys cys ser val leu ser ser val
141  10 15 20
142  tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc      211
143  tyr ala leu val asp ala asp asp val ile thr lys glu glu gln ile
144  25 30 35

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147		40					45				50						
148	gtc	ctc	agg	gtc	cct	gaa	ctt	gct	gaa	tct	gcc	aaa	gac	tgg	atg	tca	307
149	Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	Ser	
150		55				60					65				70		
151	agg	tct	gca	aag	aca	aag	aag	gag	aaa	cct	gca	gaa	aag	ctt	tat	ccc	355
152	Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
153					75					80					85		
154	cag	gca	gag	gag	tcc	agg	gaa	gtt	tct	gac	agg	agc	cgg	ctg	cag	gat	403
155	Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
156				90					95					100			
157	ggc	ttc	tgc	cta	cct	gag	tgg	gac	aac	att	gtg	tgc	tgg	cct	gct	gga	451
158	Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	
159			105					110					115				
160	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	ttc	tac	gac	499
161	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
162			120				125					130					
163	ttc	aac	cac	aaa	ggc	cga	gcc	tat	cgg	cgc	tgt	gac	agc	aat	ggc	agc	547
164	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
165		135				140					145				150		
166	tgg	gag	ctg	gtg	cct	ggg	aac	aac	cgg	aca	tgg	gcg	aat	tac	agc	gaa	595
167	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
168					155					160					165		
169	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cgg	gaa	cgg	gaa	gtc	ttt	gat	643
170	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
171				170					175					180			
172	cgc	ctc	gga	atg	atc	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc	691
173	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
174			185					190					195				
175	ctc	act	gtg	gct	gtg	ctg	att	ctg	ggt	tac	ttt	agg	agg	tta	cat	tgc	739
176	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
177			200				205					210					
178	acc	cga	aac	tac	att	cac	atg	cat	ctc	ttc	gtg	tcc	ttt	atg	ctc	cgg	787
179	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
180		215				220					225				230		
181	gct	gta	agc	atc	ttc	atc	aag	gat	gct	gtg	ctc	tac	tcg	ggg	gtt	tcc	835
182	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
183				235						240				245			
184	aca	gat	gaa	atc	gag	cgc	atc	acc	gag	gag	gag	ctg	agg	gcc	ttc	aca	883
185	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
186				250					255					260			
187	gag	cct	ccc	cct	gct	gac	aag	gcg	ggt	ttt	gtg	ggc	tgc	aga	gtg	gcg	931
188	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
189			265					270					275				
190	gta	acc	gtc	ttc	ctt	tac	ttc	ctg	acc	acc	aac	tac	tac	tgg	atc	ctg	979
191	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
192			280				285						290				
193	gtg	gaa	ggc	ctc	tac	ctt	cac	agc	ctc	atc	ttc	atg	gct	ttt	ttc	tct	1027
194	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	

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197	Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro				
198		315	320	325	
199	gcc gtg ttt gtc gct gtg tgg gtg acc gtg agg gct aca ctg gcc aac				1123
200	Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn				
201		330	335	340	
202	act gag tgc tgg gac ctg agt tgc ggg aat aag aaa tgg atc ata cag				1171
203	Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln				
204		345	350	355	
205	gtg ccc atc ctg gca gct att gtg gtg aac ttt att ctt ttt atc aat				1219
206	Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn				
207		360	365	370	
208	ata atc aga gtc ctg gct act aaa ctc cgg gag acc aat gca ggg aga				1267
209	Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg				
210		375	380	385	390
211	tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc				1315
212	Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val				
213		395	400	405	
214	ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg				1363
215	Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro				
216		410	415	420	
217	tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa				1411
218	Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu				
219		425	430	435	
220	atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt				1459
221	Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys				
222		440	445	450	
223	ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga				1507
224	Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg				
225		455	460	465	470
226	tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt				1555
227	Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser				
228		475	480	485	
229	acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg				1603
230	Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val				
231		490	495	500	
232	gga cct cga ggg ggg ctg gcc ttg tcc ctc agc cct cga cta gct cct				1651
233	Gly Pro Arg Gly Gly Leu Ala Leu Ser Leu Ser Pro Arg Leu Ala Pro				
234		505	510	515	
235	ggg gct gga gcc agt gcc aat ggc cat cac cag ttg cct ggc tat gtg				1699
236	Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val				
237		520	525	530	
238	aag cat ggt tcc att tct gag aac tca ttg cct tca tct ggc cca gag				1747
239	Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu				
240		535	540	545	550
241	cct ggc acc aaa gat gac ggg tat ctc aat ggc tct gga ctt tat gag				1795
242	Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu				
243		555	560	565	
	cca atg gtt ggg gaa cag ccc cct cca ctc ctg gag gag gag aga gag				1843

**Please Note:**

Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/199,874

DATE: 03/10/2000  
TIME: 15:41:06

Input Set: I199874.RAW

Line ? Error/Warning

Original Text

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543 W "N" or "Xaa" used: Feature required

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